

SEQUENCE LISTING



<110> Dattwyler, Raymond J.
Seinost, Gerald
Dykhuisen, Danial
Luft, Benjamin J.
Maria J.C. Gomes-Solecki

<120> Groups of Borrelia burgdorferi and
Borrelia afzelii That Cause Lyme Disease in Humans

<130> 2631.1002-001

<150> US 60/140,042

<151> 1999-06-18

<160> 84

<170> FastSEQ for Windows Version 4.0

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<220>

<223> Primer

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<210> 2

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<220>

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<400> 2

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ttgtagcag gagcttatgc aatata

26

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<212> DNA

<213> Artificial Sequence

AI
Comit

46
2/102

<220>
<223> Primer

<400> 4
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22

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Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
1 5 10 15

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
20 25 30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
35 40 45

ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata 192
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile
50 55 60

aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg 240
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
65 70 75 80

tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt 288
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser
85 90 95

aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag 336
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys
100 105 110

aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag 384
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln
115 120 125

ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta 432
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu
130 135 140

aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag 480
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys
145 150 155 160

ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt 528
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu
165 170 175

AI
Cm.t

47
3/102

gct aat tca gtt aaa gag ctt aca agc cct gtt gtc cat gga tcc 573
Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Ser
180 185 190

<210> 6
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<212> PRT
<213> borrelia burgdorferi

<400> 6
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Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
35 40 45
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile
50 55 60
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
65 70 75 80
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser
85 90 95
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys
100 105 110
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln
115 120 125
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu
130 135 140
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys
145 150 155 160
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu
165 170 175
Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Ser
180 185 190

<210> 7
<211> 557
<212> DNA
<213> Borrelia burgdorferi

<220>
<221> CDS
<222> (1)...(557)

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gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
20 25 30

AI
Cm.t

48
4/102

att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag acc 144
Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr
35 40 45

tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aaa aaa 192
Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys
50 55 60

ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca ttg 240
Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu
65 70 75 80

tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta aat 288
Leu Ser Gly Ala Tyr 85 Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn 95

gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag caa 336
Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln
100 105 110

tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg ctt 384
Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu
115 120 125

ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta aaa 432
Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys
130 135 140

aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta ttt 480
Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe
145 150 155 160

aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa aat 528
Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn
165 170 175

gct gtt aaa gag ctt aca agt cct att gt 557
Ala Val Lys Glu Leu Thr Ser Pro Ile
180 185

<210> 8

<211> 185

<212> PRT

<213> Borrelia burgdorferi

<400> 8

Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser
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Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
20 25 30
Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr
35 40 45
Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys
50 55 60
Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu
65 70 75 80
Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn
85 90 95

Al
Cm.t

49
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Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln
100 105 110
Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu
115 120 125
Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys
130 135 140
Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe
145 150 155 160
Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn
165 170 175
Ala Val Lys Glu Leu Thr Ser Pro Ile
180 185

<210> 9
<211> 579
<212> DNA
<213> Borrelia burgdorferi

<220>
<221> CDS
<222> (1)...(579)

<400> 9
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1 5 10 15
aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt 96
Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
20 25 30
aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta ctt gct 144
Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu Ala
35 40 45
gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att gct gct 192
Val Lys Glu Val Glu Ala Leu Ser Ser Ile Asp Glu Ile Ala Ala
50 55 60
aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat acc gaa 240
Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp Thr Glu
65 70 75 80
aat aat cac aat gga tca ttg tta gcg gga gct tat gca ata tca acc 288
Asn Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr
85 90 95
cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta aag gaa 336
Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu
100 105 110
aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat aaa tta 384
Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu
115 120 125
aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat gct gat 432
Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Ala Asp
130 135 140

AI
Cm.t

50
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gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa ggt gct	480
Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala	
145 150 155 160	
gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca aaa gca	528
Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser Lys Ala	
165 170 175	
gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc cct gtt	576
Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val	
180 185 190	
gtg	579
Val	

<210> 10
 <211> 193
 <212> PRT
 <213> Borrelia burgdorferi

<400> 10

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20 25 30	
Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu Ala	
35 40 45	
Val Lys Glu Val Glu Ala Leu Ser Ser Ile Asp Glu Ile Ala Ala	
50 55 60	
Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp Thr Glu	
65 70 75 80	
Asn Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr	
85 90 95	
Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu	
100 105 110	
Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu	
115 120 125	
Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Ala Asp	
130 135 140	
Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala	
145 150 155 160	
Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser Lys Ala	
165 170 175	
Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val	
180 185 190	
Val	

<210> 11
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 <212> DNA
 <213> Borrelia brgdorferi

<220>
 <221> CDS

AI
 Cm.t

<222> (1)...(582)

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1 5 10 15
aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt 96
Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
20 25 30
aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta ctt gct 144
Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu Ala
35 40 45
gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt gct aaa 192
Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys
50 55 60
gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat gaa gca 240
Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala
65 70 75 80
aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca acc tta 288
Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu
85 90 95
ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta aag gaa 336
Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu
100 105 110
aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act aaa cta 384
Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu
115 120 125
aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat gaa aat 432
Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp Glu Asn
130 135 140
gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat aag ggc 480
Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly
145 150 155 160
gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta tca aaa 528
Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys
165 170 175
gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc cct 576
Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro
180 185 190
gtt gtg 582
Val Val

<210> 12
<211> 194
<212> PRT

AI
Cm. x

52
-8/102

<213> Borrelia brgdorferi

<400> 12

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20 25 30
Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu Leu Ala
35 40 45
Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys
50 55 60
Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala
65 70 75 80
Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu
85 90 95
Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu
100 105 110
Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu
115 120 125
Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp Glu Asn
130 135 140
Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly
145 150 155 160
Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys
165 170 175
Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro
180 185 190
Val Val

<210> 13

<211> 576

<212> DNA

<213> Borrelia burgdorferi

<220>

<221> CDS

<222> (1)...(576)

<400> 13

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1 5 10 15
aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt 96
Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
20 25 30
aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gcc 144
Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala
35 40 45
gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt gct acc 192
Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr
50 55 60

53
-9/102

aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc aat cag	240
Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln	
65 70 75 80	
agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct gac cta	288
Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu	
85 90 95	
ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag gaa aag	336
Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys	
100 105 110	
att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa cta aaa	384
Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys	
115 120 125	
agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat aat gca	432
Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala	
130 135 140	
caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt gct gca	480
Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala	
145 150 155 160	
gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa gca gct	528
Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala	
165 170 175	
caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct att gtg	576
Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile Val	
180 185 190	

<210> 14
<211> 192
<212> PRT
<213> Borrelia burgdorferi

<400> 14

Met Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly	
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Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala	
35 40 45	
Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr	
50 55 60	
Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln	
65 70 75 80	
Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu	
85 90 95	
Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys	
100 105 110	
Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys	
115 120 125	
Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala	
130 135 140	

AI
Con.t

54
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Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala
145 150 155 160
Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala
165 170 175
Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile Val
180 185 190

<210> 15
<211> 576
<212> DNA
<213> borrelia burgdorferi

<220>
<221> CDS
<222> (1)...(576)

AI
cm.t

<400> 15
atg act tta ttt tta ttt ata tct tgt aat aat tca aga aaa gat ggg 48
Met Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Arg Lys Asp Gly
1 5 10 15
aat gca tct aca aat tct gcc gat gag tct gtt aaa ggg cct aat ctt 96
Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
20 25 30
aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gcc 144
Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala
35 40 45
gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt gct acc 192
Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr
50 55 60
aaa gct att ggt aag aaa ata ggc aat aat ggt tta gag gcc aat cag 240
Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln
65 70 75 80
agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct gac cta 288
Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu
85 90 95
ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag gaa aag 336
Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys
100 105 110
att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa cta aaa 384
Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys
115 120 125
agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat aat gca 432
Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala
130 135 140
caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt gct gca 480
Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala
145 150 155 160

55
11/102

gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa gca gct 528
Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala
165 170 175

caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct att gtg 576
Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile Val
180 185 190

<210> 16
<211> 192
<212> PRT
<213> borrelia burgdorferi

<400> 16
Met Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Arg Lys Asp Gly
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Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
20 25 30
Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala
35 40 45
Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr
50 55 60
Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln
65 70 75 80
Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu
85 90 95
Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys
100 105 110
Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys
115 120 125
Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala
130 135 140
Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala
145 150 155 160
Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala
165 170 175
Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro Ile Val
180 185 190

<210> 17
<211> 573
<212> DNA
<213> Borrelia burgdorferi

<220>
<221> CDS
<222> (1) ... (573)

<400> 17
atg act tta ttt tta ttt ata tct tgt aat aat tca ggg aaa gat ggg 48
Met Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly
1 5 10 15
aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt 96
Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
20 25 30

Al
cm.t

56
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aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctc gcc	144
Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala	
35 40 45	
gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat gag ctt gct aaa	192
Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys	
50 55 60	
gct att ggt aaa aaa ata aaa aac gat gtt agt tta gat aat gag gca	240
Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala	
65 70 75 80	
gat cac aac gga tca tta ata tca gga gca tat tta att tca aac tta	288
Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu	
85 90 95	
ata aca aaa aaa ata agt gca ata aaa gat tca gga gaa ttg aag gca	336
Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala	
100 105 110	
gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt act gct aaa tta	384
Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu	
115 120 125	
aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt act gat gat aat	432
Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn	
130 135 140	
gca aaa aaa gcc att tta aaa aca aat aat gat aaa act aag ggc gct	480
Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala	
145 150 155 160	
gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa gca	528
Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala	
165 170 175	
gct aaa gag atg ctt act aat tca gtt aaa gag ctt aca agc cct	573
Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser Pro	
180 185 190	

<210> 18
<211> 191
<212> PRT
<213> Borrelia burgdorferi

<400> 18

Met Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly	
1 5 10 15	
Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu	
20 25 30	
Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala	
35 40 45	
Val Lys Glu Val Glu Thr Leu Thr Ser Ile Asp Glu Leu Ala Lys	
50 55 60	
Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala	
65 70 75 80	

AI
Cm't

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Asp	His	Asn	Gly	Ser	Leu	Ile	Ser	Gly	Ala	Tyr	Leu	Ile	Ser	Asn	Leu
				85					90					95	
Ile	Thr	Lys	Lys	Ile	Ser	Ala	Ile	Lys	Asp	Ser	Gly	Glu	Leu	Lys	Ala
			100					105					110		
Glu	Ile	Glu	Lys	Ala	Lys	Lys	Cys	Ser	Glu	Glu	Phe	Thr	Ala	Lys	Leu
			115				120					125			
Lys	Gly	Glu	His	Thr	Asp	Leu	Gly	Lys	Glu	Gly	Val	Thr	Asp	Asp	Asn
			130			135					140				
Ala	Lys	Lys	Ala	Ile	Leu	Lys	Thr	Asn	Asn	Asp	Lys	Thr	Lys	Gly	Ala
					150					155					160
Asp	Glu	Leu	Glu	Lys	Leu	Phe	Glu	Ser	Val	Lys	Asn	Leu	Ser	Lys	Ala
				165					170					175	
Ala	Lys	Glu	Met	Leu	Thr	Asn	Ser	Val	Lys	Glu	Leu	Thr	Ser	Pro	
			180					185					190		

<210> 19
 <211> 553
 <212> DNA
 <213> Borrelia burgdorferi

<220>
 <221> CDS
 <222> (1)...(553)

<400> 19																
atg	act	tta	ttt	tta	ttt	ata	tct	tgt	aat	aat	tca	gga	aaa	gat	ggg	48
Met	Thr	Leu	Phe	Leu	Phe	Ile	Ser	Cys	Asn	Asn	Ser	Gly	Lys	Asp	Gly	
1				5					10					15		
aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt															96	
Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn	Leu	
			20					25					30			
aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gct															144	
Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Glu	Ser	Asn	Ala	Val	Val	Leu	Ala	
			35			40					45					
gtg aaa gaa att gaa act ttg ctt gca tct ata gat gaa ctt gct act															192	
Val	Lys	Glu	Ile	Glu	Thr	Leu	Leu	Ala	Ser	Ile	Asp	Glu	Leu	Ala	Thr	
		50				55				60						
aaa gct att ggt aaa aaa ata gat aac aat gct ggt ttg ggt gct gaa															240	
Lys	Ala	Ile	Gly	Lys	Lys	Ile	Asp	Asn	Asn	Ala	Gly	Leu	Gly	Ala	Glu	
		65			70				75					80		
gtg ggt caa aac gga tca ttg cta gca gga gct tat gca atc tca act															288	
Val	Gly	Gln	Asn	Gly	Ser	Leu	Leu	Ala	Gly	Ala	Tyr	Ala	Ile	Ser	Thr	
				85				90					95			
gta ata ata gaa aaa ttg agc aca tta aaa aat gta gaa gaa tta aaa															336	
Val	Ile	Ile	Glu	Lys	Leu	Ser	Thr	Leu	Lys	Asn	Val	Glu	Glu	Leu	Lys	
			100					105					110			
gaa aaa att aca aag gct aag gat tgt tct gaa aaa ttc act aaa aaa															384	
Glu	Lys	Ile	Thr	Lys	Ala	Lys	Asp	Cys	Ser	Glu	Lys	Phe	Thr	Lys	Lys	
			115				120					125				

Alt
cm

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tta aaa gat agc cgc gca gag ctt ggt aaa aaa gat gcc agt gat gat	432
Leu Lys Asp Ser Arg Ala Glu Leu Gly Lys Lys Asp Ala Ser Asp Asp	
130 135 140	
gat gca aaa aaa gct att tta aaa aca aat caa gct aac gat aag ggt	480
Asp Ala Lys Lys Ala Ile Leu Lys Thr Asn Gln Ala Asn Asp Lys Gly	
145 150 155 160	
gct aaa gaa ctt aaa gag tta ttt gaa gca gta gaa agc ttg tca aaa	528
Ala Lys Glu Leu Lys Glu Leu Phe Glu Ala Val Glu Ser Leu Ser Lys	
165 170 175	
gcg gct aaa gag atg cta aac aag t	553
Ala Ala Lys Glu Met Leu Asn Lys	
180	

Al
emit

<210> 20
<211> 184
<212> PRT
<213> Borrelia burgdorferi

<400> 20															
Met	Thr	Leu	Phe	Leu	Phe	Ile	Ser	Cys	Asn	Asn	Ser	Gly	Lys	Asp	Gly
1				5					10					15	
Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn	Leu
			20					25					30		
Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Glu	Ser	Asn	Ala	Val	Val	Leu	Ala
		35					40					45			
Val	Lys	Glu	Ile	Glu	Thr	Leu	Leu	Ala	Ser	Ile	Asp	Glu	Leu	Ala	Thr
	50					55				60					
Lys	Ala	Ile	Gly	Lys	Lys	Ile	Asp	Asn	Asn	Ala	Gly	Leu	Gly	Ala	Glu
65					70				75						80
Val	Gly	Gln	Asn	Gly	Ser	Leu	Leu	Ala	Gly	Ala	Tyr	Ala	Ile	Ser	Thr
			85						90					95	
Val	Ile	Ile	Glu	Lys	Leu	Ser	Thr	Leu	Lys	Asn	Val	Glu	Glu	Leu	Lys
			100					105					110		
Glu	Lys	Ile	Thr	Lys	Ala	Lys	Asp	Cys	Ser	Glu	Lys	Phe	Thr	Lys	Lys
		115					120					125			
Leu	Lys	Asp	Ser	Arg	Ala	Glu	Leu	Gly	Lys	Lys	Asp	Ala	Ser	Asp	Asp
		130				135					140				
Asp	Ala	Lys	Lys	Ala	Ile	Leu	Lys	Thr	Asn	Gln	Ala	Asn	Asp	Lys	Gly
145					150					155					160
Ala	Lys	Glu	Leu	Lys	Glu	Leu	Phe	Glu	Ala	Val	Glu	Ser	Leu	Ser	Lys
				165					170						175
Ala	Ala	Lys	Glu	Met	Leu	Asn	Lys								
				180											

<210> 21
<211> 582
<212> DNA
<213> Borrelia burgdorferi

<220>
<221> CDS
<222> (1)...(582)

<400> 21

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atg act tta ttt tta ttt ata tct tgt aat aat tca gga aaa gat ggg	48
Met Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly	
1 5 10 15	
aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt	96
Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu	
20 25 30	
aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gct	144
Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala	
35 40 45	
gtg aaa gaa att gaa act ttg ctt gca tct ata gat gaa ctt gct act	192
Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr	
50 55 60	
aaa gct att ggt aaa aaa ata caa caa aat ggt ggt tta gct gtc gaa	240
Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu	
65 70 75 80	
gcg ggg cat aat gga aca ttg tta gca ggt gct tat aca ata tca aaa	288
Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys	
85 90 95	
cta ata aca caa aaa tta gat gga ttg aaa aat tca gaa aaa tta aag	336
Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys	
100 105 110	
gaa aaa att gaa aat gct aag aaa tgt tct gaa gat ttt act aaa aaa	384
Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys	
115 120 125	
cta gaa gga gaa cat gcg caa ctt gga att gaa aat gtt act gat gag	432
Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu	
130 135 140	
aat gca aaa aaa gct att tta ata aca gat gca gct aaa gat aag ggc	480
Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly	
145 150 155 160	
gct gca gag ctt gaa aag cta ttt aaa gca gta gaa aac ttg gca aaa	528
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys	
165 170 175	
gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agt cct	576
Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro	
180 185 190	
att gtg	582
Ile Val	

<210> 22
 <211> 194
 <212> PRT
 <213> Borrelia burgdorferi
 <400> 22

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Cm.t

60
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Met Thr Leu Phe Leu Phe Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly
1 5 10 15
Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu
20 25 30
Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala
35 40 45
Val Lys Glu Ile Glu Thr Leu Ala Ser Ile Asp Glu Leu Ala Thr
50 55 60
Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu
65 70 75 80
Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys
85 90 95
Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys
100 105 110
Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys
115 120 125
Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu
130 135 140
Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly
145 150 155 160
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys
165 170 175
Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser Pro
180 185 190
Ile Val

<210> 23
<211> 1128
<212> DNA
<213> Artificial Sequence

<220>
<223> OspC Chimera

<221> CDS
<222> (1)...(1128)

<400> 23
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
1 5 10 15
gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
20 25 30
att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
35 40 45
ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
50 55 60

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ata cac caa aat aat ggt ttg gat acc gaa tat aat cac aat gga tca	240
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser	
65 70 75 80	
ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta	288
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu	
85 90 95	
gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag	336
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys	
100 105 110	
aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat	384
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp	
115 120 125	
ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta	432
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu	
130 135 140	
aaa aca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta	480
Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu	
145 150 155 160	
ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct	528
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala	
165 170 175	
aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca gcc	576
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala	
180 185 190	
atg gta aat aat tca ggg aaa gat ggg aat aca tct gca aat tct gct	624
Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala	
195 200 205	
gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa att	672
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile	
210 215 220	
aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa gtt gaa act ttg	720
Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu	
225 230 235 240	
ctt aca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata aaa	768
Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys	
245 250 255	
aac gat gtt agt tta gat aat gag gca gat cac aac gga tca tta ata	816
Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile	
260 265 270	
tca gga gca tat tta att tca aac tta ata aca aaa aaa ata agt gca	864
Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala	
275 280 285	
ata aaa gat tca gga gaa ttg aag gca gaa att gaa aag gct aag aaa	912
Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys	
290 295 300	

Al
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62
18/102

tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa cac aca gat ctt 960
 Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu 320
 305 310 315
 ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa gcc att tta aaa 1008
 Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys 335
 325 330
 aca aat aat gat aaa act aag ggc gct gat gaa ctt gaa aag tta ttt 1056
 Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe 350
 340 345
 gaa tca gta aaa aac ttg tca aaa gca gct aaa gag atg ctt act aat 1104
 Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn 365
 355 360
 tca gtt aaa gag ctt aca agc taa 1128
 Ser Val Lys Glu Leu Thr Ser *
 370 375

<210> 24
 <211> 375
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> OspC Chimera

<400> 24
 Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
 1 5 10 15
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20 25 30
 Ile Thr Asp Ser Asn Ala Val Leu Ala Val Lys Glu Val Glu Ala
 35 40 45
 Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
 50 55 60
 Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser
 65 70 75 80
 Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
 85 90 95
 Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
 100 105 110
 Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
 115 120 125
 Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
 130 135 140
 Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
 145 150 155 160
 Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
 165 170 175
 Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala
 180 185 190
 Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala
 195 200 205
 Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile
 210 215 220

AI
Cm't

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Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu
225 230 235 240
Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys
245 250 255
Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile
260 265 270
Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala
275 280 285
Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys
290 295 300
Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu
305 310 315 320
Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys
325 330 335
Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe
340 345 350
Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn
355 360 365
Ser Val Lys Glu Leu Thr Ser
370 375

<210> 25
<211> 1124
<212> DNA
<213> Artificial Sequence

<220>
<223> OspC Chimera

<221> CDS
<222> (1)...(1124)

<400> 25
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
1 5 10 15
gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
20 25 30
att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
35 40 45
ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
50 55 60
ata cac caa aat aat ggt ttg gat acc gaa tat aat cac aat gga tca 240
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser
65 70 75 80
ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 288
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
85 90 95

AI
Cm.t

64
207102

gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
100 105 110

aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 384
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
115 120 125

ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 432
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
130 135 140

aaa aca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 480
Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
145 150 155 160

ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 528
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
165 170 175

aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca gcc 576
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala
180 185 190

atg gta aat aat tca gga aaa gat ggg aat aca tct gca aat tct gct 624
Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala
195 200 205

gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa att 672
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile
210 215 220

aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa att gaa act ttg 720
Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu
225 230 235 240

ctt gca tct ata gat gaa ctt gct act aaa gct att ggt aaa aaa ata 768
Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile
245 250 255

caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat aat gga aca ttg 816
Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu
260 265 270

tta gca ggt gct tat aca ata tca aaa cta ata aca caa aaa tta gat 864
Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp
275 280 285

gga ttg aaa aat tca gaa aaa tta aag gaa aaa att gaa aat gct aag 912
Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys
290 295 300

aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga gaa cat gcg caa 960
Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln
305 310 315 320

ctt gga att gaa aat gtt act gat gag aat gca aaa aaa gct att tta 1008
Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu
325 330 335

A1
cm.t

65
-21/102

ata aca gat gca gct aaa gat aag ggc gct gca gag ctt gaa aag cta 1056
Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu
340 345 350

ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag atg ctt gct 1104
Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala
355 360 365

aat tca gtt aaa gag ctt ac 1124
Asn Ser Val Lys Glu Leu
370

<210> 26
<211> 374
<212> PRT
<213> Artificial Sequence

<220>
<223> OspC Chimera

<400> 26
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
1 5 10 15
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
20 25 30
Ile Thr Asp Ser Asn Ala Val Leu Ala Val Lys Glu Val Glu Ala
35 40 45
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
50 55 60
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser
65 70 75 80
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
85 90 95
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
100 105 110
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
115 120 125
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
130 135 140
Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
145 150 155 160
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
165 170 175
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala
180 185 190
Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala
195 200 205
Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile
210 215 220
Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu
225 230 235 240
Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile
245 250 255
Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu
260 265 270
Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp
275 280 285

AI
Cm't

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Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys
290 295 300
Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln
305 310 315 320
Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu
325 330 335
Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu
340 345 350
Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala
355 360 365
Asn Ser Val Lys Glu Leu
370

<210> 27
<211> 1137
<212> DNA
<213> Artificial Sequence

<220>
<223> OspC Chimera

<221> CDS
<222> (1)...(1137)

<400> 27
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
1 5 10 15
gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata aat aaa aaa 96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys
20 25 30
att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
35 40 45
ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
50 55 60
ata cac caa aat aat ggt ttg gat acc gaa aat aat cac aat gga tca 240
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser
65 70 75 80
ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 288
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
85 90 95
gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
100 105 110
aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 384
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
115 120 125

AI
Cm.t

67
23/102

ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta	432
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu	
130 135 140	
aaa gca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta	480
Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu	
145 150 155 160	
ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct	528
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala	
165 170 175	
aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca aaa	576
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys	
180 185 190	
aaa cct tcc atg gta aat aat tca ggg aaa gat ggg aat aca tct gca	624
Lys Pro Ser Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala	
195 200 205	
aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt	672
Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser	
210 215 220	
aaa aaa att aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa gtt	720
Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val	
225 230 235 240	
gaa act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt aaa	768
Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys	
245 250 255	
aaa ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac gga	816
Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly	
260 265 270	
tca tta ata tca gga gca tat tta att tca aac tta ata aca aaa aaa	864
Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys	
275 280 285	
ata agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa aag	912
Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys	
290 295 300	
gct aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa cac	960
Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His	
305 310 315 320	
aca gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa gcc	1008
Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala	
325 330 335	
att tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt gaa	1056
Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu	
340 345 350	
aag tta ttt gaa tca gta aaa aac ttg tca aaa gca gct aaa gag atg	1104
Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met	
355 360 365	

Al
Cm.t

68
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ctt act aat tca gtt aaa gag ctt aca agc taa
Leu Thr Asn Ser Val Lys Glu Leu Thr Ser *
370 375

1137

<210> 28
<211> 378
<212> PRT
<213> Artificial Sequence

<220>
<223> OspC Chimera

<400> 28
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
1 5 10 15
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys
20 25 30
Ile Thr Asp Ser Asn Ala Val Leu Ala Val Lys Glu Val Glu Ala
35 40 45
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
50 55 60
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser
65 70 75 80
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
85 90 95
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
100 105 110
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
115 120 125
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
130 135 140
Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Leu Gly Lys Leu
145 150 155 160
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
165 170 175
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys
180 185 190
Lys Pro Ser Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala
195 200 205
Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser
210 215 220
Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val
225 230 235 240
Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys
245 250 255
Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly
260 265 270
Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys
275 280 285
Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys
290 295 300
Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His
305 310 315 320
Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala
325 330 335
Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu
340 345 350

AI
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Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met
355 360 365
Leu Thr Asn Ser Val Lys Glu Leu Thr Ser
370 375

<210> 29
<211> 1133
<212> DNA
<213> Artificial Sequence

<220>
<223> OspC Chimera

<221> CDS
<222> (1)...(1133)

AI
omit

<400> 29
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
1 5 10 15
gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata aat aaa aaa 96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys
20 25 30
att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
Ile Thr Asp Ser Asn Ala Val Leu Ala Val Lys Glu Val Glu Ala
35 40 45
ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
50 55 60
ata cac caa aat aat ggt ttg gat acc gaa aat aat cac aat gga tca 240
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser
65 70 75 80
ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 288
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
85 90 95
gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
100 105 110
aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 384
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
115 120 125
ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 432
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
130 135 140
aaa gca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 480
Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
145 150 155 160

70
26/102

ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala 165 170 175	528
aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca aaa Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys 180 185 190	576
aaa cct tcc atg gta aat aat tca gga aaa gat ggg aat aca tct gca Lys Pro Ser Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala 195 200 205	624
aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser 210 215 220	672
aaa aaa att aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa att Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile 225 230 235 240	720
gaa act ttg ctt gca tct ata gat gaa ctt gct act aaa gct att ggt Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly 245 250 255	768
aaa aaa ata caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat aat Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn 260 265 270	816
gga aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca caa Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln 275 280 285	864
aaa tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att gaa Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu 290 295 300	912
aat gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga gaa Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu 305 310 315 320	960
cat gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa aaa His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys 325 330 335	1008
gct att tta ata aca gat gca gct aaa gat aag ggc gct gca gag ctt Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu 340 345 350	1056
gaa aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu 355 360 365	1104
atg ctt gct aat tca gtt aaa gag ctt ac Met Leu Ala Asn Ser Val Lys Glu Leu 370 375	1133

<210> 30
<211> 377

AI
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27/102

<212> PRT
<213> Artificial Sequence

<220>
<223> OspC Chimera

<400> 30
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
1 5 10 15
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys
20 25 30
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
35 40 45
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
50 55 60
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser
65 70 75 80
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
85 90 95
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Lys
100 105 110
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
115 120 125
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
130 135 140
Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
145 150 155 160
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
165 170 175
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys
180 185 190
Lys Pro Ser Met Val Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala
195 200 205
Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser
210 215 220
Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile
225 230 235 240
Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly
245 250 255
Lys Lys Ile Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn
260 265 270
Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln
275 280 285
Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu
290 295 300
Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu
305 310 315 320
His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys
325 330 335
Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu
340 345 350
Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu
355 360 365
Met Leu Ala Asn Ser Val Lys Glu Leu
370 375

<210> 31
<211> 1112

<212> DNA
<213> Artificial Sequence

<220>
<223> OspC Chimera

<221> CDS
<222> (1)...(1112)

<400> 31

atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct	48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser	
1 5 10 15	
gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa	96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys	
20 25 30	
att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg	144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala	
35 40 45	
ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata	192
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile	
50 55 60	
aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg	240
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu	
65 70 75 80	
tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt	288
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser	
85 90 95	
aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag	336
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys	
100 105 110	
aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag	384
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln	
115 120 125	
ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta	432
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu	
130 135 140	
aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag	480
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys	
145 150 155 160	
ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt	528
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu	
165 170 175	
gct aat tca gtt aaa gag ctt aca agc cct gtt gtc cat ggt aat aat	576
Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn	
180 185 190	

AI
Cm.t

tca aga aaa gat ggg aat gca tct aca aat tct gcc gat gag tct gtt 624
 Ser Arg Lys Asp Gly Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val
 195 200 205

aaa ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac 672
 Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn
 210 215 220

gca gtt gtt ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata 720
 Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile
 225 230 235 240

gat gaa ctt gct acc aaa gct att ggt aag aaa ata ggc aat aat ggt 768
 Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly
 245 250 255

tta gag gcc aat cag agt aaa aac aca tca ttg tta tca gga gct tat 816
 Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr
 260 265 270

gca ata tct gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa 864
 Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu
 275 280 285

gaa tta aag gaa aag att gat aca gct aag caa tgt tct aca gaa ttt 912
 Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe
 290 295 300

act aat aaa cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt 960
 Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu
 305 310 315 320

act gat gat aat gca caa aga gct att tta aaa aaa cat gca aat aaa 1008
 Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys
 325 330 335

gat aag ggt gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac 1056
 Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn
 340 345 350

tta tca aaa gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt 1104
 Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu
 355 360 365

aca agt cc 1112
 Thr Ser
 370

<210> 32

<211> 370

<212> PRT

<213> Artificial Sequence

<220>

<223> OspC Chimera

<400> 32

AI
omit

74
20/102

Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
1 5 10 15
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
20 25 30
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
35 40 45
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile
50 55 60
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
65 70 75 80
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser
85 90 95
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys
100 105 110
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln
115 120 125
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu
130 135 140
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys
145 150 155 160
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu
165 170 175
Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn
180 185 190
Ser Arg Lys Asp Gly Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val
195 200 205
Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn
210 215 220
Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile
225 230 235 240
Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly
245 250 255
Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr
260 265 270
Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu
275 280 285
Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe
290 295 300
Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu
305 310 315 320
Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys
325 330 335
Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn
340 345 350
Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu
355 360 365
Thr Ser
370

<210> 33
<211> 1113
<212> DNA
<213> Artificial Sequence

<220>
<223> OspC Chimera

AI
omit

75
~~31/102~~

<221> CDS
 <222> (1)...(1113)

<400> 33

atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct	48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser	
1 5 10 15	
gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa	96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys	
20 25 30	
att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg	144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala	
35 40 45	
ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata	192
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile	
50 55 60	
aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg	240
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu	
65 70 75 80	
tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt	288
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser	
85 90 95	
aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag	336
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys	
100 105 110	
aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag	384
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln	
115 120 125	
ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta	432
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu	
130 135 140	
aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag	480
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys	
145 150 155 160	
ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt	528
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu	
165 170 175	
gct aat tca gtt aaa gag ctt aca agc cct gtt gtc cat ggt aat aat	576
Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn	
180 185 190	
tca ggg aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt	624
Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val	
195 200 205	
aaa ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac	672
Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn	
210 215 220	

AI
 cm it

gca gtt gtt ctc gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata	720
Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile	
225 230 235 240	
gat gag ctt gct aaa gct att ggt aaa aaa ata aaa aac gat gtt agt	768
Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser	
245 250 255	
tta gat aat gag gca gat cac aac gga tca tta ata tca gga gca tat	816
Leu Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr	
260 265 270	
tta att tca aac tta ata aca aaa aaa ata agt gca ata aaa gat tca	864
Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser	
275 280 285	
gga gaa ttg aag gca gaa att gaa aag gct aag aaa tgt tct gaa gaa	912
Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu	
290 295 300	
ttt act gct aaa tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc	960
Phe Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly	
305 310 315 320	
gtt act gat gat aat gca aaa aaa gcc att tta aaa aca aat aat gat	1008
Val Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp	
325 330 335	
aaa act aag ggc gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa	1056
Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys	
340 345 350	
aac ttg tca aaa gca gct aaa gag atg ctt act aat tca gtt aaa gag	1104
Asn Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu	
355 360 365	
ctt aca agc	1113
Leu Thr Ser	
370	

<210> 34
 <211> 371
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> OspC Chimera

<400> 34
 Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
 1 5 10 15
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20 25 30
 Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
 35 40 45
 Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile
 50 55 60

AI
 cm.it

Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
 65 70 75 80
 Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser
 85 90 95
 Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Lys
 100 105 110
 Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln
 115 120 125
 Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu
 130 135 140
 Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys
 145 150 155 160
 Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu
 165 170 175
 Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn
 180 185 190
 Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val
 195 200 205
 Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn
 210 215 220
 Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile
 225 230 235 240
 Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser
 245 250 255
 Leu Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr
 260 265 270
 Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser
 275 280 285
 Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu
 290 295 300
 Phe Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly
 305 310 315 320
 Val Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp
 325 330 335
 Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys
 340 345 350
 Asn Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu
 355 360 365
 Leu Thr Ser
 370

<210> 35

<211> 1112

<212> DNA

<213> Artificial Sequence

<220>

<223> OspC Chimera

<221> CDS

<222> (1)...(1112)

<400> 35

atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct
 Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
 1 5 10 15

48

78
34/102

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa	96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys	
20 25 30	
att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg	144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala	
35 40 45	
ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata	192
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile	
50 55 60	
aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg	240
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu	
65 70 75 80	
tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt	288
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser	
85 90 95	
aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag	336
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys	
100 105 110	
aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag	384
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln	
115 120 125	
ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta	432
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu	
130 135 140	
aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag	480
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys	
145 150 155 160	
ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt	528
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu	
165 170 175	
gct aat tca gtt aaa gag ctt aca agc cct gtt gtc cat ggt aat aat	576
Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn	
180 185 190	
tca gga aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt	624
Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val	
195 200 205	
aaa ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac	672
Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn	
210 215 220	
gca gtt gtt ctg gct gtg aaa gaa att gaa act ttg ctt gca tct ata	720
Ala Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile	
225 230 235 240	
gat gaa ctt gct act aaa gct att ggt aaa aaa ata caa caa aat ggt	768
Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly	
245 250 255	

AI
omit

79
35/102

ggt tta gct gtc gaa gcg ggg cat aat gga aca ttg tta gca ggt gct 816
Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala
260 265 270

tat aca ata tca aaa cta ata aca caa aaa tta gat gga ttg aaa aat 864
Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn
275 280 285

tca gaa aaa tta aag gaa aaa att gaa aat gct aag aaa tgt tct gaa 912
Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu
290 295 300

gat ttt act aaa aaa cta gaa gga gaa cat gcg caa ctt gga att gaa 960
Asp Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu
305 310 315 320

aat gtt act gat gag aat gca aaa aaa gct att tta ata aca gat gca 1008
Asn Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala
325 330 335

gct aaa gat aag ggc gct gca gag ctt gaa aag cta ttt aaa gca gta 1056
Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val
340 345 350

gaa aac ttg gca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa 1104
Glu Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys
355 360 365

gag ctt ac 1112
Glu Leu
370

<210> 36
<211> 370
<212> PRT
<213> Artificial Sequence

<220>
<223> OspC Chimera

<400> 36
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
1 5 10 15
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
20 25 30
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
35 40 45
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile
50 55 60
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
65 70 75 80
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser
85 90 95
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys
100 105 110
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln
115 120 125

Al
Cm.it

80
26/102

Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu
130 135 140
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys
145 150 155 160
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu
165 170 175
Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn
180 185 190
Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val
195 200 205
Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn
210 215 220
Ala Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile
225 230 235 240
Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly
245 250 255
Gly Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala
260 265 270
Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn
275 280 285
Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu
290 295 300
Asp Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu
305 310 315 320
Asn Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala
325 330 335
Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val
340 345 350
Glu Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys
355 360 365
Glu Leu
370

<210> 37
<211> 1106
<212> DNA
<213> Artificial Sequence

<220>
<223> OspC Chimera

<221> CDS
<222> (1)...(1106)

<400> 37
atg gct tgt aat aat tca gga aaa gat ggg aat gca tct gca aat tct 48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser
1 5 10 15
gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
20 25 30
att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag acc 144
Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr
35 40 45

AI
cm.t

81
37/102

tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aaa aaa	192
Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys	
50 55 60	
ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca ttg	240
Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu	
65 70 75 80	
tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta aat	288
Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn	
85 90 95	
gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag caa	336
Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln	
100 105 110	
tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg ctt	384
Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu	
115 120 125	
ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta aaa	432
Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys	
130 135 140	
aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta ttt	480
Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe	
145 150 155 160	
aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa aat	528
Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn	
165 170 175	
gct gtt aaa gag ctt aca agt cct att gtc cat ggt aat aat tca aga	576
Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Arg	
180 185 190	
aaa gat ggg aat gca tct aca aat tct gcc gat gag tct gtt aaa ggg	624
Lys Asp Gly Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val Lys Gly	
195 200 205	
cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt	672
Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val	
210 215 220	
ggt ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa	720
Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu	
225 230 235 240	
ctt gct acc aaa gct att ggt aag aaa ata ggc aat aat ggt tta gag	768
Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu	
245 250 255	
gcc aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata	816
Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile	
260 265 270	
tct gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta	864
Ser Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu	
275 280 285	

AI
com.t

aag gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat	912
Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn	
290 295 300	
aaa cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat	960
Lys Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp	
305 310 315 320	
gat aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag	1008
Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys	
325 330 335	
ggt gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca	1056
Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser	
340 345 350	
aaa gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt	1104
Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser	
355 360 365	
cc	1106

AI
 cm.t

<210> 38
 <211> 368
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> OspC Chimera

<400> 38
 Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser
 1 5 10 15
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20 25 30
 Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr
 35 40 45
 Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys
 50 55 60
 Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu
 65 70 75 80
 Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn
 85 90 95
 Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln
 100 105 110
 Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu
 115 120 125
 Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys
 130 135 140
 Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe
 145 150 155 160
 Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn
 165 170 175
 Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Arg
 180 185 190
 Lys Asp Gly Asn Ala Ser Thr Asn Ser Ala Asp Glu Ser Val Lys Gly
 195 200 205

Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val
 210 215 220
 Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu
 225 230 235 240
 Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu
 245 250 255
 Ala Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile
 260 265 270
 Ser Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu
 275 280 285
 Lys Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn
 290 295 300
 Lys Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp
 305 310 315 320
 Asp Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys
 325 330 335
 Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser
 340 345 350
 Lys Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser
 355 360 365

AI
 cm.t

<210> 39
 <211> 1107
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> OspC Chimera

<221> CDS
 <222> (1)...(1107)

<400> 39
 atg gct tgt aat aat tca gga aaa gat ggg aat gca tct gca aat tct 48
 Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser
 1 5 10 15
 gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20 25 30
 att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag acc 144
 Ile Thr Glu Ser Asn Ala Val Leu Ala Val Lys Glu Val Glu Thr
 35 40 45
 tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aaa aaa 192
 Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys
 50 55 60
 ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca ttg 240
 Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu
 65 70 75 80
 tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta aat 288
 Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn
 85 90 95

84
40/102

gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag caa	336
Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln	
100 105 110	
tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg ctt	384
Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu	
115 120 125	
ggc ctg gac aat ctt act gat gat aat gca caa aga gct att tta aaa	432
Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys	
130 135 140	
aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta ttt	480
Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe	
145 150 155 160	
aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa aat	528
Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn	
165 170 175	
gct gtt aaa gag ctt aca agt cct att gtc cat ggt aat aat tca ggg	576
Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Gly	
180 185 190	
aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg	624
Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly	
195 200 205	
cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt	672
Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val	
210 215 220	
ggt ctc gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat gag	720
Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu	
225 230 235 240	
ctt gct aaa gct att ggt aaa aaa ata aaa aac gat gtt agt tta gat	768
Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp	
245 250 255	
aat gag gca gat cac aac gga tca tta ata tca gga gca tat tta att	816
Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile	
260 265 270	
tca aac tta ata aca aaa aaa ata agt gca ata aaa gat tca gga gaa	864
Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu	
275 280 285	
ttg aag gca gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt act	912
Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr	
290 295 300	
gct aaa tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt act	960
Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr	
305 310 315 320	
gat gat aat gca aaa aaa gcc att tta aaa aca aat aat gat aaa act	1008
Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr	
325 330 335	

AI
Em.t

85
41/102

aag ggc gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac ttg 1056
Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu
340 345 350

tca aaa gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt aca 1104
Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr
355 360 365

agc
Ser

1107

<210> 40
<211> 369
<212> PRT
<213> Artificial Sequence

<220>
<223> OspC Chimera

<400> 40
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser
1 5 10 15
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
20 25 30
Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr
35 40 45
Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys
50 55 60
Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu
65 70 75 80
Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn
85 90 95
Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln
100 105 110
Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu
115 120 125
Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys
130 135 140
Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe
145 150 155 160
Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn
165 170 175
Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Gly
180 185 190
Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly
195 200 205
Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val
210 215 220
Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu
225 230 235 240
Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp
245 250 255
Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile
260 265 270
Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu
275 280 285

AI
Commit

86
42/102

Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr
 290 295 300
 Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr
 305 310 315 320
 Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr
 325 330 335
 Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu
 340 345 350
 Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr
 355 360 365
 Ser

<210> 41
 <211> 1106
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> OspC Chimera

<221> CDS
 <222> (1)...(1106)

<400> 41
 atg gct tgt aat aat tca gga aaa gat ggg aat gca tct gca aat tct 48
 Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser
 1 5 10 15
 gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
 Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
 20 25 30
 att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag acc 144
 Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr
 35 40 45
 tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aaa aaa 192
 Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys
 50 55 60
 ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca ttg 240
 Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu
 65 70 75 80
 tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta aat 288
 Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn
 85 90 95
 gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag caa 336
 Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln
 100 105 110
 tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg ctt 384
 Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu
 115 120 125

AI
 Unit

87
43/102

ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta aaa	432
Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu Lys	
130 135 140	
aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta ttt	480
Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe	
145 150 155 160	
aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa aat	528
Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn	
165 170 175	
gct gtt aaa gag ctt aca agt cct att gtc cat ggt aat aat tca gga	576
Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Gly	
180 185 190	
aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg	624
Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly	
195 200 205	
cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt	672
Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val	
210 215 220	
ggt ctg gct gtg aaa gaa att gaa act ttg ctt gca tct ata gat gaa	720
Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu	
225 230 235 240	
ctt gct act aaa gct att ggt aaa aaa ata caa caa aat ggt ggt tta	768
Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu	
245 250 255	
gct gtc gaa gcg ggg cat aat gga aca ttg tta gca ggt gct tat aca	816
Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr	
260 265 270	
ata tca aaa cta ata aca caa aaa tta gat gga ttg aaa aat tca gaa	864
Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu	
275 280 285	
aaa tta aag gaa aaa att gaa aat gct aag aaa tgt tct gaa gat ttt	912
Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe	
290 295 300	
act aaa aaa cta gaa gga gaa cat gcg caa ctt gga att gaa aat gtt	960
Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val	
305 310 315 320	
act gat gag aat gca aaa aaa gct att tta ata aca gat gca gct aaa	1008
Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys	
325 330 335	
gat aag ggc gct gca gag ctt gaa aag cta ttt aaa gca gta gaa aac	1056
Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn	
340 345 350	
ttg gca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt	1104
Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu	
355 360 365	

Al
cont

ac

<210> 42
<211> 368
<212> PRT
<213> Artificial Sequence

<220>
<223> OspC Chimera

<400> 42
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Ala Ser Ala Asn Ser
1 5 10 15
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
20 25 30
Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr
35 40 45
Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys
50 55 60
Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser Leu
65 70 75 80
Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu Asn
85 90 95
Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys Gln
100 105 110
Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val Leu
115 120 125
Gly Leu Asp Asn Leu Thr Asp Asn Ala Gln Arg Ala Ile Leu Lys
130 135 140
Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe
145 150 155 160
Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys Asn
165 170 175
Ala Val Lys Glu Leu Thr Ser Pro Ile Val His Gly Asn Asn Ser Gly
180 185 190
Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly
195 200 205
Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val
210 215 220
Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu
225 230 235 240
Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu
245 250 255
Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr
260 265 270
Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu
275 280 285
Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe
290 295 300
Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val
305 310 315 320
Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys
325 330 335
Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn
340 345 350
Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu
355 360 365

AI
cm.t

<210> 43
<211> 633
<212> DNA
<213> Borrelia burgdorferi

<220>
<221> CDS
<222> (1)...(633)

<400> 43
atg aaa aag aat aca tta agt gcg ata tta atg act tta ttt tta ttt 48
Met Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe
1 5 10 15

ata tct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 96
Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
20 25 30

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata aat aaa aaa 144
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys
35 40 45

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 192
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
50 55 60

ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 240
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
65 70 75 80

ata cac caa aat aat ggt ttg gat acc gaa aat aat cac aat gga tca 288
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser
85 90 95

ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 336
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
100 105 110

gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 384
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
115 120 125

aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 432
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
130 135 140

ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 480
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
145 150 155 160

aaa gca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 528
Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
165 170 175

ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 576
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
180 185 190

AI
Cm.t

90
46/102

aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca aaa 624
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys
195 200 205

aaa cct taa
Lys Pro *
210

633

<210> 44
<211> 210
<212> PRT
<213> Borrelia burgdorferi

<400> 44
Met Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe
1 5 10 15
Ile Ser Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
20 25 30
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys
35 40 45
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
50 55 60
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
65 70 75 80
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser
85 90 95
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
100 105 110
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
115 120 125
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
130 135 140
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
145 150 155 160
Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
165 170 175
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
180 185 190
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys
195 200 205
Lys Pro
210

<210> 45
<211> 580
<212> DNA
<213> Borrelia burgdorferi

<220>
<221> CDS
<222> (1)...(580)

<400> 45
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
1 5 10 15

91
47/102

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata aat aaa aaa 96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys
20 25 30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
35 40 45

ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
50 55 60

ata cac caa aat aat ggt ttg gat acc gaa aat aat cac aat gga tca 240
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser
65 70 75 80

ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta 288
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
85 90 95

gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag 336
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
100 105 110

aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat 384
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
115 120 125

ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta 432
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
130 135 140

aaa gca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta 480
Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
145 150 155 160

ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct 528
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
165 170 175

aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca tcc 576
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ser
180 185 190

atg g 580
Met

<210> 46
<211> 193
<212> PRT
<213> Borrelia burgdorferi

<400> 46
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
1 5 10 15
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Asn Lys Lys
20 25 30

AI
Com't

92
48/102

Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
 35 40 45
 Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
 50 55 60
 Ile His Gln Asn Asn Gly Leu Asp Thr Glu Asn Asn His Asn Gly Ser
 65 70 75 80
 Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
 85 90 95
 Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
 100 105 110
 Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
 115 120 125
 Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
 130 135 140
 Lys Ala Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
 145 150 155 160
 Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
 165 170 175
 Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ser
 180 185 190
 Met

AI
cm.t

<210> 47
 <211> 639
 <212> DNA
 <213> Borrelia garinii

<220>
 <221> CDS
 <222> (1)...(639)

<400> 47
 atg aaa aag aat aca tta agt gcg ata tta atg act tta ttt tta ttt 48
 Met Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe
 1 5 10 15
 ata tct tgt agt aat tca ggg aaa ggt ggg gat tct gca tct act aat 96
 Ile Ser Cys Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn
 20 25 30
 cct gct gac gag tct gcg aaa ggg cct aat ctt aca gaa ata agc aaa 144
 Pro Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys
 35 40 45
 aaa att aca gat tct aat gca ttt gta ctt gct gtt aaa gaa gtt gag 192
 Lys Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu
 50 55 60
 act ttg gtt tta tct ata gat gaa ctt gct aag aaa gct att ggt caa 240
 Thr Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln
 65 70 75 80
 aaa ata gac aat aat aat ggt tta gct gct tta aat aat cag aat gga 288
 Lys Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly
 85 90 95

93
49/102

tcg ttg tta gca gga gcc tat gca ata tca acc cta ata aca gaa aaa 336
Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys
100 105 110

ttg agt aaa ttg aaa aat tta gaa gaa tta aag aca gaa att gca aag 384
Leu Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys
115 120 125

gct aag aaa tgt tcc gaa gaa ttt act aat aaa cta aaa agt ggt cat 432
Ala Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His
130 135 140

gca gat ctt ggc aaa cag gat gct acc gat gat cat gca aaa gca gct 480
Ala Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala
145 150 155 160

att tta aaa aca cat gca act acc gat aaa ggt gct aaa gaa ttt aaa 528
Ile Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys
165 170 175

gat tta ttt gaa tca gta gaa ggt ttg tta aaa gca gct caa gta gca 576
Asp Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala
180 185 190

cta act aat tca gtt aaa gaa ctt aca agt cct gtt gta gca gaa agt 624
Leu Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser
195 200 205

cca aaa aaa cct taa 639
Pro Lys Lys Pro *

<210> 48
<211> 212
<212> PRT
<213> Borrelia garinii

<400> 48
Met Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe
1 5 10 15
Ile Ser Cys Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn
20 25 30
Pro Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys
35 40 45
Lys Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu
50 55 60
Thr Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln
65 70 75 80
Lys Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly
85 90 95
Ser Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys
100 105 110
Leu Ser Lys Leu Lys Asn Leu Glu Leu Lys Thr Glu Ile Ala Lys
115 120 125
Ala Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His
130 135 140
Ala Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala
145 150 155 160

AI
Cm.t

94
50/102

Ile Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys
165 170 175
Asp Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala
180 185 190
Leu Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser
195 200 205
Pro Lys Lys Pro
210

<210> 49
<211> 624
<212> DNA
<213> Borrelia afzelii

<220>
<221> CDS
<222> (1)...(624)

<400> 49
atg aaa aag aat aca tta agt gcg ata tta atg act tta ttt tta ttt 48
Met Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe
1 5 10 15
ata tct tgt aat aat tca ggt ggg gat tct gca tct act aat cct gat 96
Ile Ser Cys Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp
20 25 30
gag tct gca aaa gga cct aat ctt acc gta ata agc aaa aaa att aca 144
Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr
35 40 45
gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag gct ttg ctt 192
Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu
50 55 60
tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa ata aaa aat 240
Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn
65 70 75 80
gat ggt act tta gat aac gaa gca aat cga aac gaa tca ttg ata gca 288
Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala
85 90 95
gga gct tat gaa ata tca aaa cta ata aca caa aaa tta agt gta ttg 336
Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu
100 105 110
aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag gat tgt tcc 384
Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser
115 120 125
caa aaa ttt act act aag cta aaa gat agt cat gca gag ctt ggt ata 432
Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile
130 135 140
caa agc gtt cag gat gat aat gca aaa aaa gct att tta aaa aca cat 480
Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His
145 150 155 160

AI
Cm. +

95
51/102

gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta ttt aaa tca 528
Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser
165 170 175

cta gaa agc ttg tca aaa gca gcg caa gca gca tta act aat tca gtt 576
Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val
180 185 190

aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa aaa cct taa 624
Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro *
195 200 205

<210> 50
<211> 207
<212> PRT
<213> Borrelia afzelii

<400> 50
Met Lys Lys Asn Thr Leu Ser Ala Ile Leu Met Thr Leu Phe Leu Phe
1 5 10 15
Ile Ser Cys Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp
20 25 30
Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr
35 40 45
Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu
50 55 60
Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn
65 70 75 80
Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala
85 90 95
Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu
100 105 110
Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser
115 120 125
Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile
130 135 140
Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His
145 150 155 160
Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser
165 170 175
Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val
180 185 190
Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro
195 200 205

<210> 51
<211> 1680
<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1680)

<400> 51

AI
omit

96
52/102

atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct	48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser	
1 5 10 15	
gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa	96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys	
20 25 30	
att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg	144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala	
35 40 45	
ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa	192
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys	
50 55 60	
ata cac caa aat aat ggt ttg gat acc gaa tat aat cac aat gga tca	240
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser	
65 70 75 80	
ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta	288
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu	
85 90 95	
gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag	336
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys	
100 105 110	
aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat	384
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp	
115 120 125	
ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta	432
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu	
130 135 140	
aaa aca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta	480
Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu	
145 150 155 160	
ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct	528
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala	
165 170 175	
aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca gcc	576
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala	
180 185 190	
atg ggt agt aat tca ggg aaa ggt ggg gat tct gca tct act aat cct	624
Met Gly Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn Pro	
195 200 205	
gct gac gag tct gcg aaa ggg cct aat ctt aca gaa ata agc aaa aaa	672
Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys	
210 215 220	
att aca gat tct aat gca ttt gta ctt gct gtt aaa gaa gtt gag act	720
Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr	
225 230 235 240	

Al
mit

97
53/102

ttg gtt tta tct ata gat gaa ctt gct aag aaa gct att ggt caa aaa	768
Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys	
245 250 255	
ata gac aat aat aat ggt tta gct gct tta aat aat cag aat gga tcg	816
Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser	
260 265 270	
ttg tta gca gga gcc tat gca ata tca acc cta ata aca gaa aaa ttg	864
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu	
275 280 285	
agt aaa ttg aaa aat tta gaa gaa tta aag aca gaa att gca aag gct	912
Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys Ala	
290 295 300	
aag aaa tgt tcc gaa gaa ttt act aat aaa cta aaa agt ggt cat gca	960
Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala	
305 310 315 320	
gat ctt ggc aaa cag gat gct acc gat gat cat gca aaa gca gct att	1008
Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile	
325 330 335	
tta aaa aca cat gca act acc gat aaa ggt gct aaa gaa ttt aaa gat	1056
Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp	
340 345 350	
tta ttt gaa tca gta gaa ggt ttg tta aaa gca gct caa gta gca cta	1104
Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu	
355 360 365	
act aat tca gtt aaa gaa ctt ggt cac cgt aat aat tca ggt ggg gat	1152
Thr Asn Ser Val Lys Glu Leu Gly His Arg Asn Asn Ser Gly Gly Asp	
370 375 380	
tct gca tct act aat cct gat gag tct gca aaa gga cct aat ctt acc	1200
Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr	
385 390 395 400	
gta ata agc aaa aaa att aca gat tct aat gca ttt tta ctg gct gtg	1248
Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val	
405 410 415	
aaa gaa gtt gag gct ttg ctt tca tct ata gat gaa ctt tct aaa gct	1296
Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala	
420 425 430	
att ggt aaa aaa ata aaa aat gat ggt act tta gat aac gaa gca aat	1344
Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn	
435 440 445	
cga aac gaa tca ttg ata gca gga gct tat gaa ata tca aaa cta ata	1392
Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile	
450 455 460	

AI
Com.T

98
-54/102

aca caa aaa tta agt gta ttg aat tca gaa gaa tta aag aaa aaa att 1440
Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile
465 470 475 480

aaa gag gct aag gat tgt tcc caa aaa ttt act act aag cta aaa gat 1488
Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp
485 490 495

agt cat gca gag ctt ggt ata caa agc gtt cag gat gat aat gca aaa 1536
Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys
500 505 510

aaa gct att tta aaa aca cat gga act aaa gac aag ggt gct aaa gaa 1584
Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu
515 520 525

ctt gaa gag tta ttt aaa tca cta gaa agc ttg tca aaa gca gcg caa 1632
Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln
530 535 540

gca gca tta act aat tca gtt aaa gag ctt aca aat cct gtt gtg gca 1680
Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala
545 550 555 560

<210> 52
<211> 560
<212> PRT
<213> ospC Chimera

<400> 52
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
1 5 10 15
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
20 25 30
Ile Thr Asp Ser Asn Ala Val Leu Ala Val Lys Glu Val Glu Ala
35 40 45
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
50 55 60
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser
65 70 75 80
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
85 90 95
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
100 105 110
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
115 120 125
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
130 135 140
Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
145 150 155 160
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
165 170 175
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Ala
180 185 190
Met Gly Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn Pro
195 200 205

A1
Cm.T

99
55/102

Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
210 215 220
Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr
225 230 235 240
Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys
245 250 255
Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser
260 265 270
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu
275 280 285
Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys Ala
290 295 300
Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala
305 310 315 320
Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile
325 330 335
Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp
340 345 350
Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu
355 360 365
Thr Asn Ser Val Lys Glu Leu Gly His Arg Asn Asn Ser Gly Gly Asp
370 375 380
Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr
385 390 395 400
Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val
405 410 415
Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala
420 425 430
Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn
435 440 445
Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile
450 455 460
Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile
465 470 475 480
Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp
485 490 495
Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys
500 505 510
Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu
515 520 525
Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln
530 535 540
Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala
545 550 555 560

<210> 53
<211> 1137
<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1137)

<400> 53
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
1 5 10 15

100
56/102

gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
20 25 30

att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
35 40 45

ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata 192
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile
50 55 60

aaa aac gat ggt agt tta gat aat gaa gca aat cgc aac gag tca ttg 240
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
65 70 75 80

tta gca gga gct tat aca ata tca acc tta ata aca caa aaa tta agt 288
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser
85 90 95

aaa tta aac gga tca gaa ggt tta aag gaa aag att gcc gca gct aag 336
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys
100 105 110

aaa tgc tct gaa gag ttt agt act aaa cta aaa gat aat cat gca cag 384
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln
115 120 125

ctt ggt ata cag ggc gtt act gat gaa aat gca aaa aaa gct att tta 432
Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu
130 135 140

aaa gca aat gca gcg ggt aaa gat aag ggc gtt gaa gaa ctt gaa aag 480
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys
145 150 155 160

ttg tcc gga tca tta gaa agc tta tca aaa gca gct aaa gag atg ctt 528
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu
165 170 175

gct aat tca gtt aaa gag ctt aca agc cct gtt gtc cat ggt aat aat 576
Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn
180 185 190

tca ggt ggg gat tct gca tct act aat cct gat gag tct gca aaa gga 624
Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly
195 200 205

cct aat ctt acc gta ata agc aaa aaa att aca gat tct aat gca ttt 672
Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe
210 215 220

tta ctg gct gtg aaa gaa gtt gag gct ttg ctt tca tct ata gat gaa 720
Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu
225 230 235 240

AI
cm.t

161
57/102

ctt tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta gat 768
Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp
245 250 255

aac gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa ata 816
Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile
260 265 270

tca aaa cta ata aca caa aaa tta agt gta ttg aat tca gaa gaa tta 864
Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu
275 280 285

aag aaa aaa att aaa gag gct aag gat tgt tcc caa aaa ttt act act 912
Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr
290 295 300

aag cta aaa gat agt cat gca gag ctt ggt ata caa agc gtt cag gat 960
Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp
305 310 315 320

gat aat gca aaa aaa gct att tta aaa aca cat gga act aaa gac aag 1008
Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys
325 330 335

ggt gct aaa gaa ctt gaa gag tta ttt aaa tca cta gaa agc ttg tca 1056
Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser
340 345 350

aaa gca gcg caa gca gca tta act aat tca gtt aaa gag ctt aca aat 1104
Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn
355 360 365

cct gtt gtg gca gaa agt cca aaa aaa cct taa 1137
Pro Val Val Ala Glu Ser Pro Lys Lys Pro *

<210> 54
<211> 378
<212> PRT
<213> ospC Chimera

<400> 54
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
1 5 10 15
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
20 25 30
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
35 40 45
Leu Leu Ser Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile
50 55 60
Lys Asn Asp Gly Ser Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
65 70 75 80
Leu Ala Gly Ala Tyr Thr Ile Ser Thr Leu Ile Thr Gln Lys Leu Ser
85 90 95
Lys Leu Asn Gly Ser Glu Gly Leu Lys Glu Lys Ile Ala Ala Ala Lys
100 105 110
Lys Cys Ser Glu Glu Phe Ser Thr Lys Leu Lys Asp Asn His Ala Gln
115 120 125

AI
Cm't

162
58/102

Leu Gly Ile Gln Gly Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu
130 135 140
Lys Ala Asn Ala Ala Gly Lys Asp Lys Gly Val Glu Glu Leu Glu Lys
145 150 155 160
Leu Ser Gly Ser Leu Glu Ser Leu Ser Lys Ala Ala Lys Glu Met Leu
165 170 175
Ala Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val His Gly Asn Asn
180 185 190
Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly
195 200 205
Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe
210 215 220
Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu
225 230 235 240
Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp
245 250 255
Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile
260 265 270
Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu
275 280 285
Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr
290 295 300
Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp
305 310 315 320
Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys
325 330 335
Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser
340 345 350
Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn
355 360 365
Pro Val Val Ala Glu Ser Pro Lys Lys Pro
370 375

<210> 55
<211> 1158
<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1158)

<400> 55
atg gct tgt aat aat tca ggg aaa gat ggg aat aca tct gca aat tct 48
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
1 5 10 15
gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa 96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
20 25 30
att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg 144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
35 40 45
ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa 192
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
50 55 60

103
~~59/102~~

ata cac caa aat aat ggt ttg gat acc gaa tat aat cac aat gga tca Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser 65 70 75 80	240
ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu 85 90 95	288
gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys 100 105 110	336
aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp 115 120 125	384
ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu 130 135 140	432
aaa aca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu 145 150 155 160	480
ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala 165 170 175	528
aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca aaa Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys 180 185 190	576
aaa cct ttc cat ggt aat aat tca ggt ggg gat tct gca tct act aat Lys Pro Phe His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn 195 200 205	624
cct gat gag tct gca aaa gga cct aat ctt acc gta ata agc aaa aaa Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys 210 215 220	672
att aca gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag gct Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala 225 230 235 240	720
ttg ctt tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa ata Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile 245 250 255	768
aaa aat gat ggt act tta gat aac gaa gca aat cga aac gaa tca ttg Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu 260 265 270	816
ata gca gga gct tat gaa ata tca aaa cta ata aca caa aaa tta agt Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser 275 280 285	864

A1
 cm.t

164
60/102

gta ttg aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag gat 912
Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp
290 295 300

tgt tcc caa aaa ttt act act aag cta aaa gat agt cat gca gag ctt 960
Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu
305 310 315 320

ggt ata caa agc gtt cag gat gat aat gca aaa aaa gct att tta aaa 1008
Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys
325 330 335

aca cat gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta ttt 1056
Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe
340 345 350

aaa tca cta gaa agc ttg tca aaa gca gcg caa gca gca tta act aat 1104
Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn
355 360 365

tca gtt aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa aaa 1152
Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys
370 375 380

cct taa 1158
Pro *
385

<210> 56
<211> 385
<212> PRT
<213> ospC Chimera

<400> 56
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser
1 5 10 15
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
20 25 30
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala
35 40 45
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys
50 55 60
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser
65 70 75 80
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
85 90 95
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
100 105 110
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
115 120 125
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
130 135 140
Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
145 150 155 160
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
165 170 175
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys
180 185 190

A1
cm.t

165
61/102

Lys Pro Phe His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn
195 200 205
Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys
210 215 220
Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala
225 230 235 240
Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile
245 250 255
Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
260 265 270
Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser
275 280 285
Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp
290 295 300
Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu
305 310 315 320
Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys
325 330 335
Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe
340 345 350
Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn
355 360 365
Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys
370 375 380
Pro
385

<210> 57
<211> 1161
<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1161)

<400> 57
atg tgt agt aat tca ggg aaa ggt ggg gat tct gca tct act aat cct 48
Met Cys Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn Pro
1 5 10 15
gct gac gag tct gcg aaa ggg cct aat ctt aca gaa ata agc aaa aaa 96
Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
20 25 30
att aca gat tct aat gca ttt gta ctt gct gtt aaa gaa gtt gag act 144
Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr
35 40 45
ttg gtt tta tct ata gat gaa ctt gct aag aaa gct att ggt caa aaa 192
Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys
50 55 60
ata gac aat aat aat ggt tta gct gct tta aat aat cag aat gga tcg 240
Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser
65 70 75 80

AI
cm. x

166
62/102

ttg tta gca gga gcc tat gca ata tca acc cta ata aca gaa aaa ttg	288
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu	
85 90 95	
agt aaa ttg aaa aat tta gaa gaa tta aag aca gaa att gca aag gct	336
Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys Ala	
100 105 110	
aag aaa tgt tcc gaa gaa ttt act aat aaa cta aaa agt ggt cat gca	384
Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala	
115 120 125	
gat ctt ggc aaa cag gat gct acc gat gat cat gca aaa gca gct att	432
Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile	
130 135 140	
tta aaa aca cat gca act acc gat aaa ggt gct aaa gaa ttt aaa gat	480
Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp	
145 150 155 160	
tta ttt gaa tca gta gaa ggt ttg tta aaa gca gct caa gta gca cta	528
Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu	
165 170 175	
act aat tca gtt aaa gaa ctt aca agt cct gtt gta gca gaa agt cca	576
Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro	
180 185 190	
aaa aaa cct cat atg gct aat aat tca ggt ggg gat tct gca tct act	624
Lys Lys Pro His Met Ala Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr	
195 200 205	
aat cct gat gag tct gca aaa gga cct aat ctt acc gta ata agc aaa	672
Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys	
210 215 220	
aaa att aca gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag	720
Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu	
225 230 235 240	
gct ttg ctt tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa	768
Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys	
245 250 255	
ata aaa aat gat ggt act tta gat aac gaa gca aat cga aac gaa tca	816
Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser	
260 265 270	
ttg ata gca gga gct tat gaa ata tca aaa cta ata aca caa aaa tta	864
Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu	
275 280 285	
agt gta ttg aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag	912
Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys	
290 295 300	
gat tgt tcc caa aaa ttt act act aag cta aaa gat agt cat gca gag	960
Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu	
305 310 315 320	

A1
com.t

167
63/102

ctt ggt ata caa agc gtt cag gat gat aat gca aaa aaa gct att tta 1008
Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu
325 330 335

aaa aca cat gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta 1056
Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu
340 345 350

ttt aaa tca cta gaa agc ttg tca aaa gca gcg caa gca gca tta act 1104
Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr
355 360 365

aat tca gtt aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa 1152
Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys
370 375 380

aaa cct taa 1161
Lys Pro *
385

<210> 58
<211> 386
<212> PRT
<213> ospC Chimera

<400> 58
Met Cys Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn Pro
1 5 10 15
Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys
20 25 30
Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr
35 40 45
Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys
50 55 60
Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser
65 70 75 80
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu
85 90 95
Ser Lys Leu Lys Asn Leu Glu Glu Leu Lys Thr Glu Ile Ala Lys Ala
100 105 110
Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala
115 120 125
Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile
130 135 140
Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp
145 150 155 160
Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu
165 170 175
Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro
180 185 190
Lys Lys Pro His Met Ala Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr
195 200 205
Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys
210 215 220
Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu
225 230 235 240

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Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys
245 250 255
Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser
260 265 270
Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu
275 280 285
Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys
290 295 300
Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu
305 310 315 320
Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu
325 330 335
Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu
340 345 350
Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr
355 360 365
Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys
370 375 380
Lys Pro
385

<210> 59
<211> 1197
<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1197)

<400> 59
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
65 70 75 80

gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
85 90 95

acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
100 105 110

AI
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109
~~65/102~~

tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
 115 120 125

aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat 432
 Lys Glu Lys Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn
 130 135 140

aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat 480
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp
 145 150 155 160

gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa 528
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys
 165 170 175

ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca 576
 Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser
 180 185 190

aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc 624
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
 195 200 205

cct gtt gtg gca gaa agt cca gcc atg gta aat aat tca ggg aaa gat 672
 Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp
 210 215 220

ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat 720
 Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
 225 230 235 240

ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctc 768
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu
 245 250 255

gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat gag ctt gct 816
 Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala
 260 265 270

aaa gct att ggt aaa aaa ata aaa aac gat gtt agt tta gat aat gag 864
 Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu
 275 280 285

gca gat cac aac gga tca tta ata tca gga gca tat tta att tca aac 912
 Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn
 290 295 300

tta ata aca aaa aaa ata agt gca ata aaa gat tca gga gaa ttg aag 960
 Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys
 305 310 315 320

gca gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt act gct aaa 1008
 Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys
 325 330 335

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110
66/102

tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt act gat gat 1056
Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp
340 345 350

aat gca aaa aaa gcc att tta aaa aca aat aat gat aaa act aag ggc 1104
Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly
355 360 365

gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa 1152
Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys
370 375 380

gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt aca agc 1197
Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser
385 390 395

<210> 60
<211> 399
<212> PRT
<213> ospC Chimera

<400> 60
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
1 5 10 15
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
20 25 30
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
35 40 45
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
50 55 60
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
65 70 75 80
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
85 90 95
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
100 105 110
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
115 120 125
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn
130 135 140
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp
145 150 155 160
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys
165 170 175
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser
180 185 190
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
195 200 205
Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp
210 215 220
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
225 230 235 240
Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu
245 250 255
Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala
260 265 270

AI
con.x

111
67/102

Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu
275 280 285
Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn
290 295 300
Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys
305 310 315 320
Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys
325 330 335
Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp
340 345 350
Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly
355 360 365
Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys
370 375 380
Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser
385 390 395

<210> 61
<211> 1196
<212> DNA
<213> ospC Chimera

AI
Com't

<220>
<221> CDS
<222> (1)...(1196)

<400> 61
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
1 5 10 15
gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
20 25 30
gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
35 40 45
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
50 55 60
ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
65 70 75 80
gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
85 90 95
acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
100 105 110
tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
115 120 125

aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat	432
Lys Glu Lys Ile Asp Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn	
130 135 140	
aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat	480
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp	
145 150 155 160	
gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa	528
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys	
165 170 175	
ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca	576
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser	
180 185 190	
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc	624
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser	
195 200 205	
cct gtt gtg gca gaa agt cca gcc atg gta aat aat tca gga aaa gat	672
Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp	
210 215 220	
ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat	720
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn	
225 230 235 240	
ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg	768
Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu	
245 250 255	
gct gtg aaa gaa att gaa act ttg ctt gca tct ata gat gaa ctt gct	816
Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala	
260 265 270	
act aaa gct att ggt aaa aaa ata caa caa aat ggt ggt tta gct gtc	864
Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val	
275 280 285	
gaa gcg ggg cat aat gga aca ttg tta gca ggt gct tat aca ata tca	912
Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser	
290 295 300	
aaa cta ata aca caa aaa tta gat gga ttg aaa aat tca gaa aaa tta	960
Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu	
305 310 315 320	
aag gaa aaa att gaa aat gct aag aaa tgt tct gaa gat ttt act aaa	1008
Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys	
325 330 335	
aaa cta gaa gga gaa cat gcg caa ctt gga att gaa aat gtt act gat	1056
Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp	
340 345 350	

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113
~~69/102~~

gag aat gca aaa aaa gct att tta ata aca gat gca gct aaa gat aag 1104
 Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys
 355 360 365

ggc gct gca gag ctt gaa aag cta ttt aaa gca gta gaa aac ttg gca 1152
 Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala
 370 375 380

aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt ac 1196
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu
 385 390 395

<210> 62
 <211> 398
 <212> PRT
 <213> ospC Chimera

<400> 62
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
 65 70 75 80
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
 85 90 95
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
 100 105 110
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
 115 120 125
 Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn
 130 135 140
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp
 145 150 155 160
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys
 165 170 175
 Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser
 180 185 190
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
 195 200 205
 Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp
 210 215 220
 Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
 225 230 235 240
 Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu
 245 250 255
 Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala
 260 265 270
 Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val
 275 280 285
 Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser
 290 295 300

AI
 cont

114
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Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu
305 310 315 320
Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys
325 330 335
Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp
340 345 350
Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys
355 360 365
Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala
370 375 380
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu
385 390 395

<210> 63
<211> 1185
<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1185)

<400> 63
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt 240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
65 70 75 80

gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat 288
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
85 90 95

gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca 336
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser
100 105 110

acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta 384
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu
115 120 125

aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act 432
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr
130 135 140

AI
Comit

aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat 480
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp
145 150 155 160

gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat 528
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp
165 170 175

aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta 576
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu
180 185 190

tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca 624
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr
195 200 205

agc cct gtt gtc cat ggt aat aat tca ggg aaa gat ggg aat aca tct 672
Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser
210 215 220

gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata 720
Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile
225 230 235 240

agt aaa aaa att aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa 768
Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu
245 250 255

gtt gaa act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt 816
Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly
260 265 270

aaa aaa ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac 864
Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn
275 280 285

gga tca tta ata tca gga gca tat tta att tca aac tta ata aca aaa 912
Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys
290 295 300

aaa ata agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa 960
Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu
305 310 315 320

aag gct aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa 1008
Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu
325 330 335

cac aca gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa 1056
His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys
340 345 350

gcc att tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt 1104
Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu
355 360 365

AI
Cont

116
72/102

gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa gca gct aaa gag 1152
Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu
370 375 380

atg ctt act aat tca gtt aaa gag ctt aca agc 1185
Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser
385 390 395

<210> 64
<211> 395
<212> PRT
<213> ospC Chimera

<400> 64
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
1 5 10 15
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
20 25 30
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
35 40 45
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
50 55 60
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
65 70 75 80
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
85 90 95
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser
100 105 110
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu
115 120 125
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr
130 135 140
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp
145 150 155 160
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp
165 170 175
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu
180 185 190
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr
195 200 205
Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser
210 215 220
Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile
225 230 235 240
Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu
245 250 255
Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly
260 265 270
Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn
275 280 285
Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys
290 295 300
Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu
305 310 315 320
Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu
325 330 335
His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys
340 345 350

AI
cm.t

117
23/10/2

Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu
 355 360 365
 Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu
 370 375 380
 Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser
 385 390 395

<210> 65
 <211> 1184
 <212> DNA
 <213> ospC Chimera

<220>
 <221> CDS
 <222> (1) ... (1184)

<400> 65
 atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt 240
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
 65 70 75 80

gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat 288
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
 85 90 95

gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca 336
 Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser
 100 105 110

acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta 384
 Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu
 115 120 125

aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act 432
 Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr
 130 135 140

aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat 480
 Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp
 145 150 155 160

AI
Cm it

118
74/102

gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp 165 170 175	528
aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu 180 185 190	576
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr 195 200 205	624
agc cct gtt gtc cat ggt aat aat tca gga aaa gat ggg aat aca tct Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser 210 215 220	672
gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile 225 230 235 240	720
agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu 245 250 255	768
att gaa act ttg ctt gca tct ata gat gaa ctt gct act aaa gct att Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile 260 265 270	816
ggt aaa aaa ata caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His 275 280 285	864
aat gga aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr 290 295 300	912
caa aaa tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile 305 310 315 320	960
gaa aat gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly 325 330 335	1008
gaa cat gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys 340 345 350	1056
aaa gct att tta ata aca gat gca gct aaa gat aag ggc gct gca gag Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu 355 360 365	1104
ctt gaa aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys 370 375 380	1152
gag atg ctt gct aat tca gtt aaa gag ctt ac Glu Met Leu Ala Asn Ser Val Lys Glu Leu 385 390	1184

Al
cm.t

<210> 66
<211> 394
<212> PRT
<213> ospC Chimera

<400> 66
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
1 5 10 15
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
20 25 30
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
35 40 45
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
50 55 60
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
65 70 75 80
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
85 90 95
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser
100 105 110
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu
115 120 125
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr
130 135 140
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp
145 150 155 160
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp
165 170 175
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu
180 185 190
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr
195 200 205
Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser
210 215 220
Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile
225 230 235 240
Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu
245 250 255
Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile
260 265 270
Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His
275 280 285
Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr
290 295 300
Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile
305 310 315 320
Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly
325 330 335
Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys
340 345 350
Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu
355 360 365
Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys
370 375 380
Glu Met Leu Ala Asn Ser Val Lys Glu Leu
385 390

AI
cm.t

<210> 67
<211> 1184
<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1184)

<400> 67
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt 240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
65 70 75 80

gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat 288
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
85 90 95

gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca 336
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser
100 105 110

acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta 384
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu
115 120 125

aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act 432
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr
130 135 140

aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat 480
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp
145 150 155 160

gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat 528
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp
165 170 175

aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta 576
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu
180 185 190

AI
Cm.t

121
77/102

tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr 195 200 205	624
agc cct gtt gtc cat ggt aat aat tca aga aaa gat ggg aat gca tct Ser Pro Val Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser 210 215 220	672
aca aat tct gcc gat gag tct gtt aaa ggg cct aat ctt aca gaa ata Thr Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile 225 230 235 240	720
agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu 245 250 255	768
gtt gag acc tta ctt gca tct ata gat gaa ctt gct acc aaa gct att Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile 260 265 270	816
ggg aag aaa ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn 275 280 285	864
aca tca ttg tta tca gga gct tat gca ata tct gac cta ata gca gaa Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu 290 295 300	912
aaa tta aat gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr 305 310 315 320	960
gct aag caa tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His 325 330 335	1008
gca gtg ctt ggt ctg gac aat ctt act gat gat aat gca caa aga gct Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala 340 345 350	1056
att tta aaa aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu 355 360 365	1104
aag tta ttt aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr 370 375 380	1152
tta aaa aat gct gtt aaa gag ctt aca agt cc Leu Lys Asn Ala Val Lys Glu Leu Thr Ser 385 390	1184

<210> 68
<211> 394
<212> PRT
<213> ospC Chimera

<400> 68

AI
cm't

122
78/102

Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
1 5 10 15
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
20 25 30
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
35 40 45
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
50 55 60
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
65 70 75 80
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
85 90 95
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser
100 105 110
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu
115 120 125
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr
130 135 140
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp
145 150 155 160
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp
165 170 175
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu
180 185 190
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr
195 200 205
Ser Pro Val Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser
210 215 220
Thr Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile
225 230 235 240
Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu
245 250 255
Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile
260 265 270
Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn
275 280 285
Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu
290 295 300
Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr
305 310 315 320
Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His
325 330 335
Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala
340 345 350
Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu
355 360 365
Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr
370 375 380
Leu Lys Asn Ala Val Lys Glu Leu Thr Ser
385 390

AI
Cm't

<210> 69
<211> 1209
<212> DNA
<213> ospC Chimera

<220>
<221> CDS

123
~~79/102~~

<222> (1)...(1209)

<400> 69
 atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt 240
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ile Asp Glu Leu
 65 70 75 80

gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat 288
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
 85 90 95

gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca 336
 Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser
 100 105 110

acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta 384
 Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu
 115 120 125

aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act 432
 Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr
 130 135 140

aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat 480
 Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp
 145 150 155 160

gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat 528
 Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp
 165 170 175

aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta 576
 Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu
 180 185 190

tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca 624
 Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr
 195 200 205

agc cct gtt gtc cat ggt aat aat tca ggt ggg gat tct gca tct act 672
 Ser Pro Val Val His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr
 210 215 220

AI
 cm't

124
80/102

aat cct gat gag tct gca aaa gga cct aat ctt acc gta ata agc aaa 720
Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys
225 230 235 240

aaa att aca gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag 768
Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu
245 250 255

gct ttg ctt tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa 816
Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys
260 265 270

ata aaa aat gat ggt act tta gat aac gaa gca aat cga aac gaa tca 864
Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser
275 280 285

ttg ata gca gga gct tat gaa ata tca aaa cta ata aca caa aaa tta 912
Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu
290 295 300

agt gta ttg aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag 960
Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys
305 310 315 320

gat tgt tcc caa aaa ttt act act aag cta aaa gat agt cat gca gag 1008
Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu
325 330 335

ctt ggt ata caa agc gtt cag gat gat aat gca aaa aaa gct att tta 1056
Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu
340 345 350

aaa aca cat gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta 1104
Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu
355 360 365

ttt aaa tca cta gaa agc ttg tca aaa gca gcg caa gca gca tta act 1152
Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr
370 375 380

aat tca gtt aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa 1200
Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys
385 390 395 400

aaa cct taa 1209
Lys Pro *

<210> 70
<211> 402
<212> PRT
<213> ospC Chimera

<400> 70
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
1 5 10 15
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
20 25 30

AI
Cm.T

125
81/102

Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
35 40 45
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
50 55 60
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
65 70 75 80
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
85 90 95
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser
100 105 110
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu
115 120 125
Lys Glu Lys Ile Ala Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr
130 135 140
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp
145 150 155 160
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp
165 170 175
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu
180 185 190
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr
195 200 205
Ser Pro Val Val His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr
210 215 220
Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys
225 230 235 240
Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu
245 250 255
Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys
260 265 270
Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser
275 280 285
Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu
290 295 300
Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys
305 310 315 320
Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu
325 330 335
Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu
340 345 350
Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu
355 360 365
Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr
370 375 380
Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys
385 390 395 400
Lys Pro

AI
Cm.t

<210> 71
<211> 1179
<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1179)

126
82/102

<400> 71
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa 96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
20 25 30

gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
35 40 45

aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt 192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val
50 55 60

ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt 240
Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu
65 70 75 80

gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc 288
Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala
85 90 95

aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct 336
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser
100 105 110

gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag 384
Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys
115 120 125

gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa 432
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys
130 135 140

cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat 480
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp
145 150 155 160

aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt 528
Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly
165 170 175

gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa 576
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys
180 185 190

gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct 624
Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro
195 200 205

att gtc cat ggt aat aat tca ggg aaa gat ggg aat aca tct gca aat 672
Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn
210 215 220

AI
Cmt

127
83/102

tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys 225 230 235 240	720
aaa att aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa gtt gaa Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu 245 250 255	768
act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt aaa aaa Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys 260 265 270	816
ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac gga tca Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser 275 280 285	864
tta ata tca gga gca tat tta att tca aac tta ata aca aaa aaa ata Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile 290 295 300	912
agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa aag gct Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala 305 310 315 320	960
aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa cac aca Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr 325 330 335	1008
gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa gcc att Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile 340 345 350	1056
tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt gaa aag Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys 355 360 365	1104
tta ttt gaa tca gta aaa aac ttg tca aaa gca gct aaa gag atg ctt Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu 370 375 380	1152
act aat tca gtt aaa gag ctt aca agc Thr Asn Ser Val Lys Glu Leu Thr Ser 385 390	1179

<210> 72
<211> 393
<212> PRT
<213> ospC Chimera

<400> 72
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
1 5 10 15
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
20 25 30
Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
35 40 45
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val
50 55 60

Al
Cm.t

128
84/102

Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu
65 70 75 80
Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala
85 90 95
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser
100 105 110
Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys
115 120 125
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys
130 135 140
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp
145 150 155 160
Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly
165 170 175
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys
180 185 190
Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro
195 200 205
Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn
210 215 220
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys
225 230 235 240
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu
245 250 255
Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys
260 265 270
Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser
275 280 285
Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile
290 295 300
Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala
305 310 315 320
Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr
325 330 335
Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile
340 345 350
Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys
355 360 365
Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu
370 375 380
Thr Asn Ser Val Lys Glu Leu Thr Ser
385 390

<210> 73
<211> 1178
<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1178)

<400> 73
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
1 5 10 15

AI
cm.t

129
85/102

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa 96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
20 25 30

gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
35 40 45

aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt 192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val
50 55 60

ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt 240
Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu
65 70 75 80

gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc 288
Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala
85 90 95

aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct 336
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser
100 105 110

gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag 384
Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys
115 120 125

gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa 432
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys
130 135 140

cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat 480
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp
145 150 155 160

aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt 528
Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly
165 170 175

gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa 576
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys
180 185 190

gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct 624
Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro
195 200 205

att gtc cat ggt aat aat tca gga aaa gat ggg aat aca tct gca aat 672
Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn
210 215 220

tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa 720
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys
225 230 235 240

aaa att aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa att gaa 768
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu
245 250 255

A1
cm.t

act ttg ctt gca tct ata gat gaa ctt gct act aaa gct att ggt aaa 816
Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys
260 265 270

aaa ata caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat aat gga 864
Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly
275 280 285

aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca caa aaa 912
Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys
290 295 300

tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att gaa aat 960
Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn
305 310 315 320

gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga gaa cat 1008
Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His
325 330 335

gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa aaa gct 1056
Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala
340 345 350

att tta ata aca gat gca gct aaa gat aag ggc gct gca gag ctt gaa 1104
Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu
355 360 365

aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag atg 1152
Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met
370 375 380

ctt gct aat tca gtt aaa gag ctt ac 1178
Leu Ala Asn Ser Val Lys Glu Leu
385 390

<210> 74
<211> 392
<212> PRT
<213> ospC Chimera

<400> 74
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
1 5 10 15
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
20 25 30
Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
35 40 45
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val
50 55 60
Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu
65 70 75 80
Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala
85 90 95
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser
100 105 110

AI
cm.t

131
-87/102

Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys
115 120 125
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys
130 135 140
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp
145 150 155 160
Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly
165 170 175
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys
180 185 190
Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro
195 200 205
Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn
210 215 220
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys
225 230 235 240
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu
245 250 255
Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys
260 265 270
Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly
275 280 285
Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys
290 295 300
Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn
305 310 315 320
Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His
325 330 335
Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala
340 345 350
Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu
355 360 365
Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met
370 375 380
Leu Ala Asn Ser Val Lys Glu Leu
385 390

<210> 75
<211> 1178
<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1178)

<400> 75
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys
1 5 10 15
gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa 96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
20 25 30
gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
35 40 45

AI
Comit

132
~~88/102~~

aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt 192
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val
 50 55 60

ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt 240
 Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu
 65 70 75 80

gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc 288
 Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala
 85 90 95

aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct 336
 Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser
 100 105 110

gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag 384
 Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys
 115 120 125

gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa 432
 Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys
 130 135 140

cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat 480
 Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp
 145 150 155 160

aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt 528
 Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly
 165 170 175

gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa 576
 Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys
 180 185 190

gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct 624
 Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro
 195 200 205

att gtc cat ggt aat aat tca aga aaa gat ggg aat gca tct aca aat 672
 Ile Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser Thr Asn
 210 215 220

tct gcc gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa 720
 Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys
 225 230 235 240

aaa att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag 768
 Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu
 245 250 255

acc tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aag 816
 Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys
 260 265 270

AI
 cm.t

aaa ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca 864
Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser
275 280 285

ttg tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta 912
Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu
290 295 300

aat gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag 960
Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys
305 310 315 320

caa tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg 1008
Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val
325 330 335

ctt ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta 1056
Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu
340 345 350

aaa aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta 1104
Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu
355 360 365

ttt aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa 1152
Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys
370 375 380

aat gct gtt aaa gag ctt aca agt cc 1178
Asn Ala Val Lys Glu Leu Thr Ser
385 390

<210> 76
<211> 392
<212> PRT
<213> ospC Chimera

<400> 76
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
1 5 10 15
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
20 25 30
Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
35 40 45
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val
50 55 60
Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu
65 70 75 80
Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala
85 90 95
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser
100 105 110
Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys
115 120 125
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys
130 135 140
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp
145 150 155 160

AI
Comit

134
90/102

AI
Cm't

Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly
165 170 175
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys
180 185 190
Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro
195 200 205
Ile Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser Thr Asn
210 215 220
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys
225 230 235 240
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu
245 250 255
Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys
260 265 270
Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser
275 280 285
Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu
290 295 300
Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys
305 310 315 320
Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val
325 330 335
Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu
340 345 350
Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu
355 360 365
Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys
370 375 380
Asn Ala Val Lys Glu Leu Thr Ser
385 390

<210> 77
<211> 1230
<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1230)

<400> 77
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys 15
1 5 10

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys 30
20 25 45

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu 55 60
50

135
21/102

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile 80
65 70 75

gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp 95
85 90

acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile 110
100 105

tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu 125
115 120

aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat 432
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn 140
130 135

aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat 480
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp 160
145 150 155

gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa 528
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys 175
165 170

ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca 576
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser 190
180 185

aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc 624
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser 205
195 200

cct gtt gtg gca gaa agt cca aaa aaa cct ttc cat ggt aat aat tca 672
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Phe His Gly Asn Asn Ser 220
210 215

ggt ggg gat tct gca tct act aat cct gat gag tct gca aaa gga cct 720
Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro 240
225 230 235

aat ctt acc gta ata agc aaa aaa att aca gat tct aat gca ttt tta 768
Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu 255
245 250

ctg gct gtg aaa gaa gtt gag gct ttg ctt tca tct ata gat gaa ctt 816
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu 270
260 265

tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta gat aac 864
Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn 285
275 280

gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa ata tca 912
Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser 300
290 295

AI
Cm.t

136
~~92/102~~

aaa cta ata aca caa aaa tta agt gta ttg aat tca gaa gaa tta aag 960
 Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys 320
 305 310 315

aaa aaa att aaa gag gct aag gat tgt tcc caa aaa ttt act act aag 1008
 Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys 335
 325 330

cta aaa gat agt cat gca gag ctt ggt ata caa agc gtt cag gat gat 1056
 Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp 350
 340 345

aat gca aaa aaa gct att tta aaa aca cat gga act aaa gac aag ggt 1104
 Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly 365
 355 360

gct aaa gaa ctt gaa gag tta ttt aaa tca cta gaa agc ttg tca aaa 1152
 Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys 380
 370 375

gca gcg caa gca gca tta act aat tca gtt aaa gag ctt aca aat cct 1200
 Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro 400
 385 390 395

gtt gtg gca gaa agt cca aaa aaa cct taa 1230
 Val Val Ala Glu Ser Pro Lys Lys Pro *

<210> 78
 <211> 409
 <212> PRT
 <213> ospC Chimera

<400> 78
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
 65 70 75 80
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
 85 90 95
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
 100 105 110
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
 115 120 125
 Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn
 130 135 140
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp
 145 150 155 160
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys
 165 170 175

AI
 Com't

137
93/102

AI
Com. x

Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser
180 185 190
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
195 200 205
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Phe His Gly Asn Asn Ser
210 215 220
Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro
225 230 235 240
Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu
245 250 255
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
260 265 270
Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn
275 280 285
Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser
290 295 300
Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys
305 310 315 320
Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys
325 330 335
Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp
340 345 350
Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly
355 360 365
Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys
370 375 380
Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro
385 390 395 400
Val Val Ala Glu Ser Pro Lys Lys Pro
405

<210> 79
<211> 1209
<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1209)

<400> 79
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys 15
1 5 10
gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys 30
20 25
gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro 45
35 40
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu 60
50 55

138
~~347102~~

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile 80
65 70 75

gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp 95
85 90

acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile 110
100 105

tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384
Ser Thr Leu Ile Lys Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu 125
115 120

aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat 432
Lys Glu Lys Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn 140
130 135

aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat 480
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp 160
145 150 155

gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa 528
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys 175
165 170

ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca 576
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser 190
180 185

aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc 624
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser 205
195 200

cct gtt gtg gca gaa agt cca aaa aaa cct tcc atg gta aat aat tca 672
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser 220
210 215

ggg aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa 720
Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys 240
225 230 235

ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca 768
Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala 255
245 250

gtt gtt ctc gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat 816
Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp 270
260 265

gag ctt gct aaa gct att ggt aaa aaa ata aaa aac gat gtt agt tta 864
Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu 285
275 280

gat aat gag gca gat cac aac gga tca tta ata tca gga gca tat tta 912
Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu 300
290 295

AI
Cm.t

139
95/102

att tca aac tta ata aca aaa aaa ata agt gca ata aaa gat tca gga 960
Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly 320
305 310 315

gaa ttg aag gca gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt 1008
Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe 335
325 330

act gct aaa tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt 1056
Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val 350
340 345

act gat gat aat gca aaa aaa gcc att tta aaa aca aat aat gat aaa 1104
Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys 365
355 360

act aag ggc gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac 1152
Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn 380
370 375

ttg tca aaa gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt 1200
Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu 400
385 390 395

aca agc taa 1209
Thr Ser *

<210> 80
<211> 402
<212> PRT
<213> ospC Chimera

<400> 80
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys 15
1 5 10
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys 30
20 25
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro 45
35 40
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu 60
50 55
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile 80
65 70 75
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp 95
85 90
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile 110
100 105
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu 125
115 120
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn 140
130 135
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp 160
145 150 155
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys 175
165 170

AI
Cm't

140
96/102

Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser
180 185 190
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
195 200 205
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser
210 215 220
Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys
225 230 235 240
Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala
245 250 255
Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp
260 265 270
Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu
275 280 285
Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu
290 295 300
Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly
305 310 315 320
Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe
325 330 335
Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val
340 345 350
Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys
355 360 365
Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn
370 375 380
Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu
385 390 395 400
Thr Ser

AI
Cm't

<210> 81
<211> 1205
<212> DNA
<213> ospC Chimera

<220>
<221> CDS
<222> (1)...(1205)

<400> 81
atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys 15
1 5 10
gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys 30
20 25
gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro 45
35 40
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu 60
50

141
97/102

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile 80
65 70 75

gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp 95
85 90

acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile 110
100 105

tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu 125
115 120

aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat 432
Lys Glu Lys Ile Asp Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn 140
130 135

aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat 480
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp 160
145 150 155

gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa 528
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys 175
165 170

ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca 576
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser 190
180 185

aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc 624
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser 205
195 200

cct gtt gtg gca gaa agt cca aaa aaa cct tcc atg gta aat aat tca 672
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser 220
210 215

gga aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa 720
Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys 240
225 230 235

ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca 768
Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala 255
245 250

gtt gtt ctg gct gtg aaa gaa att gaa act ttg ctt gca tct ata gat 816
Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp 270
260 265

gaa ctt gct act aaa gct att ggt aaa aaa ata caa caa aat ggt ggt 864
Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly 285
275 280

tta gct gtc gaa gcg ggg cat aat gga aca ttg tta gca ggt gct tat 912
Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr 300
290 295

AI
cm it

142
~~98/102~~

aca ata tca aaa cta ata aca caa aaa tta gat gga ttg aaa aat tca 960
 Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser 320
 305 310 315

gaa aaa tta aag gaa aaa att gaa aat gct aag aaa tgt tct gaa gat 1008
 Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp 335
 325 330

ttt act aaa aaa cta gaa gga gaa cat gcg caa ctt gga att gaa aat 1056
 Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn 350
 340 345

gtt act gat gag aat gca aaa aaa gct att tta ata aca gat gca gct 1104
 Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala 365
 355 360

aaa gat aag ggc gct gca gag ctt gaa aag cta ttt aaa gca gta gaa 1152
 Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu 380
 370 375

aac ttg gca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag 1200
 Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu 400
 385 390 395

ctt ac 1205
 Leu

AI
 Cm't

<210> 82
 <211> 401
 <212> PRT
 <213> ospC Chimera

<400> 82
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys 15
 1 5 10
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys 30
 20 25
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro 45
 35 40
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu 60
 50 55
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile 80
 65 70 75
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp 95
 85 90
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile 110
 100 105
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu 125
 115 120
 Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn 140
 130 135
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp 160
 145 150 155
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys 175
 165 170
 Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser

143
~~99/102~~

AI
 comit

Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser 180
 195
 Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser 200
 210
 Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys 215
 225
 Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala 230
 245
 Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp 250
 260
 Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly 265
 275
 Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr 280
 290
 Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser 295
 305
 Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp 310
 325
 Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn 315
 340
 Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala 330
 355
 Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu 335
 370
 Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu 345
 385
 Leu 360
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 395
 400

<210> 83
 <211> 1236
 <212> DNA
 <213> ospC Chimera

<220>
 <221> CDS
 <222> (1)...(1236)

<400> 83
 atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys 15
 1
 5
 10
 15
 20
 25
 30
 35
 40
 45
 50
 55
 60
 65
 70
 75
 80
 85
 90
 95
 100
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 115
 120
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 135
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 145
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 155
 160
 165
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 330
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 355
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 385
 390
 395
 400

144

~~100/102~~

gta ctt gct gtt aaa gaa gtt gag act ttg gtt tta tct ata gat gaa 240
Val Leu Ala Val Lys Glu Val Glu Thr Leu Val Leu Ser Ile Asp Glu 80
65 70 75

ctt gct aag aaa gct att ggt caa aaa ata gac aat aat aat ggt tta 288
Leu Ala Lys Lys Ala Ile Gly Gln Lys Ile Asp Asn Asn Asn Gly Leu 95
85 90

gct gct tta aat aat cag aat gga tct ttg tta gca gga gcc tat gca 336
Ala Ala Leu Asn Asn Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala 110
100 105

ata tca acc cta ata aca gaa aaa ttg agt aaa ttg aaa aat tta gaa 384
Ile Ser Thr Leu Ile Thr Glu Lys Leu Ser Lys Leu Lys Asn Leu Glu 125
115 120

gaa tta aag aca gaa att gca aag gct aag aaa tgt tcc gaa gaa ttt 432
Glu Leu Lys Thr Glu Ile Ala Lys Ala Lys Lys Cys Ser Glu Glu Phe 140
130 135

act aat aaa cta aaa agt ggt cat gca gat ctt ggc aaa cag gat gct 480
Thr Asn Lys Leu Lys Ser Gly His Ala Asp Leu Gly Lys Gln Asp Ala 160
145 150 155

acc gat gat cat gca aaa gca gct att tta aaa aca cat gca act acc 528
Thr Asp Asp His Ala Lys Ala Ala Ile Leu Lys Thr His Ala Thr Thr 175
165 170

gat aaa ggt gct aaa gaa ttt aaa gat tta ttt gaa tca gta gaa ggt 576
Asp Lys Gly Ala Lys Glu Phe Lys Asp Leu Phe Glu Ser Val Glu Gly 190
180 185

ttg tta aaa gca gct caa gta gca cta act aat tca gtt aaa gaa ctt 624
Leu Leu Lys Ala Ala Gln Val Ala Leu Thr Asn Ser Val Lys Glu Leu 205
195 200

aca agt cct gtt gta gca gaa agt cca aaa aaa cct cat atg gct aat 672
Thr Ser Pro Val Val Ala Glu Ser Pro Lys Lys Pro His Met Ala Asn 220
210 215

aat tca ggt ggg gat tct gca tct act aat cct gat gag tct gca aaa 720
Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys 240
225 230 235

gga cct aat ctt acc gta ata agc aaa aaa att aca gat tct aat gca 768
Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala 255
245 250

ttt tta ctg gct gtg aaa gaa gtt gag gct ttg ctt tca tct ata gat 816
Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ile Asp 270
260 265

gaa ctt tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta 864
Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu 285
275 280

gat aac gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa 912
Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu 300
290 295

AI
Cm.t

145
101/102

ata tca aaa cta ata aca caa aaa tta agt gta ttg aat tca gaa gaa 960
Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu 320
305 310 315

tta aag aaa aaa att aaa gag gct aag gat tgt tcc caa aaa ttt act 1008
Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr 335
325 330

act aag cta aaa gat agt cat gca gag ctt ggt ata caa agc gtt cag 1056
Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln 350
340 345

gat gat aat gca aaa aaa gct att tta aaa aca cat gga act aaa gac 1104
Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp 365
355 360

aag ggt gct aaa gaa ctt gaa gag tta ttt aaa tca cta gaa agc ttg 1152
Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu 380
370 375

tca aaa gca gcg caa gca gca tta act aat tca gtt aaa gag ctt aca 1200
Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr 400
385 390 395

aat cct gtt gtg gca gaa agt cca aaa aaa cct taa 1236
Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro * 410
405

<210> 84
<211> 411
<212> PRT
<213> ospC Chimera

<400> 84
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys 15
1 5 10
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Ser Asn Ser Gly Lys 30
20 25
Gly Gly Asp Ser Ala Ser Thr Asn Pro Ala Asp Glu Ser Ala Lys Gly 45
35 40
Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe 60
50 55
Val Leu Ala Val Lys Glu Val Glu Thr Leu Val Leu Ser Ile Asp Glu 80
65 70 75
Leu Ala Lys Lys Ala Ile Gly Gln Lys Ile Asp Asn Asn Asn Gly Leu 95
85 90
Ala Ala Leu Asn Asn Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala 110
100 105
Ile Ser Thr Leu Ile Thr Glu Lys Leu Ser Lys Leu Lys Asn Leu Glu 125
115 120
Glu Leu Lys Thr Glu Ile Ala Lys Ala Lys Lys Cys Ser Glu Glu Phe 140
130 135
Thr Asn Lys Leu Lys Ser Gly His Ala Asp Leu Gly Lys Gln Asp Ala 160
145 150 155
Thr Asp Asp His Ala Lys Ala Ala Ile Leu Lys Thr His Ala Thr Thr 175
165 170

Al
Cm't

146
102/102

Asp Lys Gly Ala Lys Glu Phe Lys Asp Leu Phe Glu Ser Val Glu Gly
180 185 190
Leu Leu Lys Ala Ala Gln Val Ala Leu Thr Asn Ser Val Lys Glu Leu
195 200 205
Thr Ser Pro Val Val Ala Glu Ser Pro Lys Lys Pro His Met Ala Asn
210 215 220
Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys
225 230 235 240
Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala
245 250 255
Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp
260 265 270
Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu
275 280 285
Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu
290 295 300
Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu
305 310 315 320
Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr
325 330 335
Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln
340 345 350
Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp
355 360 365
Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe Lys Ser Leu Glu Ser Leu
370 375 380
Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr
385 390 395 400
Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro
405 410

AI
Concld.